

RW

PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/868,605

DATE: 07/05/2001
TIME: 15:38:31

Input Set : A:\PTO.txt
Output Set: N:\CRF3\07032001\I868605.raw

3 <110> APPLICANT: ML Laboratories PLC
5 <120> TITLE OF INVENTION: Immunosuppression
7 <130> FILE REFERENCE: P15700WO
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/868,605
C--> 10 <141> CURRENT FILING DATE: 2001-06-19
12 <150> PRIOR APPLICATION NUMBER: 9827921.9
13 <151> PRIOR FILING DATE: 1998-12-19
15 <150> PRIOR APPLICATION NUMBER: 9925015.1
16 <151> PRIOR FILING DATE: 1999-10-23
18 <160> NUMBER OF SEQ ID NOS: 39
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 288
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
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31 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
32 20 25 30
34 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
35 35 40 45
37 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
38 50 55 60
40 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
41 65 70 75 80
43 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
44 85 90 95
46 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
47 100 105 110
49 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
50 115 120 125
52 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
53 130 135 140
55 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
56 145 150 155 160
58 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
59 165 170 175
61 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
62 180 185 190
64 Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
65 195 200 205
67 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
68 210 215 220
70 Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
71 225 230 235 240
73 Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly

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74 245 250 255
 76 Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
 77 260 265 270
 79 Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
 80 275 280 285
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 87 <211> LENGTH: 972
 88 <212> TYPE: DNA
 89 <213> ORGANISM: Homo sapiens
 91 <400> SEQUENCE: 2
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 93 aagattcaag cttatttcaa ttagactgca gacctgccat gccaatttgc aaactctcaa 120
 94 aaccaaagcc ttagttagct agtagtattt tggcaggacc agaaaaactt gttctgaat 180
 95 gaggtatact taggcaaaga gaaatttgc acgtgttcatt ccaagttat gggccgcaca 240
 96 agttttgatt cggacagttt gaccctgaga cttcacaaatc ttccatcaaa ggacaaggc 300
 97 ttgtatcaat gtatcatcca tcacaaaaag cccacaggaa tgattcgcat ccaccagatg 360
 98 aattctgaac tgcgtgtct tgcttaacttc agtcaacctg aaatagtacc aatttctaat 420
 99 ataacagaaa atgtgtacat aaatttgc acc tgctcatcta tacacggta cccagaacct 480
 100 aagaagatga gtgtttgtc aagaaccaag aattcaacta tcgagttatga tggtattatg 540
 101 cagaaatctc aagataatgt cacagaaactg tacgacgtt ccatcagctt gtctgttca 600
 102 ttccctgtatgc ttacgagcaa tatgaccatc ttctgttattc tggaaacttga caagacgcgg 660
 103 ctttatctt caccttctc tatagagctt gaggaccctc agcctcccc agaccacatt 720
 104 ccttggatta cagctgtact tccaacagtt attatatgtg tgatggttt ctgtctaatt 780
 105 ctatggaaat ggaagaagaa gaagcggctt cgcaactctt ataaatgtgg aaccaacaca 840
 106 atggagaggg aagagagtga acagaccaag aaaagagaaa aaatccatat acctgaaaga 900
 107 tctgatgaag cccagcgtgt tttaaaagt tcgaagacat cttcatgca caaaagtgtat 960
 108 acatgtttt aa 972
 111 <210> SEQ ID NO: 3
 112 <211> LENGTH: 323
 113 <212> TYPE: PRT
 114 <213> ORGANISM: Homo sapiens
 116 <400> SEQUENCE: 3
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 120 Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
 121 20 25 30
 123 Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
 124 35 40 45
 126 Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
 127 50 55 60
 129 Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
 130 65 70 75 80
 132 Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
 133 85 90 95
 135 Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr
 136 100 105 110
 138 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
 139 115 120 125
 141 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn

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142	130	135	140													
144	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	His	Gly	Tyr	Pro	Glu	Pro
145	145															160
147	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr	Ile	Glu	Tyr
148										165				170		175
150	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu	Leu	Tyr	Asp
151										180			185		190	
153	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr	Ser	Asn	Met
154										195			200		205	
156	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu	Leu	Ser	Ser
157										210			215		220	
159	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	Asp	His	Ile
160	225					230					235					240
162	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	Val	Met	Val
163										245			250		255	
165	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Arg	Pro	Arg	Asn	
166										260			265		270	
168	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu	Ser	Glu	Gln
169										275			280		285	
171	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser	Asp	Glu	Ala
172										290			295		300	
174	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser	Ser	Cys	Asp	Lys	Ser	Asp
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182	<211>	LENGTH:	834													
183	<212>	TYPE:	DNA													
184	<213>	ORGANISM:	Homo sapiens													
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188	gaaccaccca	ctgcatgcag	agaaaaaacag	tacctaataa	acagtcagt	ctgttcttg	120									
189	tgccagccag	gacagaaaact	ggtgagtgac	tgcacagagt	tcactgaaac	ggaatgcctt	180									
190	ccttgcgggt	aaagcgaatt	cctagacacc	tggAACAGAG	agacacactg	ccaccagcac	240									
191	aaataactgcg	accccaacct	agggcttcgg	gtccagcaga	agggcaccc	agaaacagac	300									
192	accatctgca	cctgtgaaga	aggctggcac	tgtacgagt	aggcctgtga	gagctgtgc	360									
193	ctgcaccgc	catgctcgcc	cggctttgg	gtcaagcaga	ttgctacagg	ggtttctgat	420									
194	accatctgcg	agccctgccc	agtccggctc	ttctccaatg	tgtcatctgc	tttcgaaaaa	480									
195	tgtcaccctt	ggacaagctg	tgagaccaa	gacctggtt	tgcaacaggc	aggcacaaac	540									
196	aagactgtat	ttgtctgtgg	tcccaggat	cggctgagag	ccctgggtgt	gatccccatc	600									
197	atttcggga	tcctgtttgc	catacctctg	gtgctggct	ttatcaaaaa	ggtggccaag	660									
198	aagccaaacca	ataaggcccc	ccaccccaag	caggaacccc	aggagatcaa	ttttccgac	720									
199	gatcttcctg	gctccaaacac	tgctgctcca	gtgcaggaga	ctttacatgg	atgccaacccg	780									
200	gtcaccagg	aggatggcaa	agagagtgc	atctcagtgc	aggagagaca	gtga	834									
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204	<211>	LENGTH:	277													
205	<212>	TYPE:	PRT													
206	<213>	ORGANISM:	Homo sapiens													
208	<400>	SEQUENCE:	5													
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210 1 5 10 15
 212 Ala Val His Pro Glu Pro Pro Thr Ala Cys Arg Glu Lys Gln Tyr Leu
 213 20 ~ 25 30
 215 Ile Asn Ser Gln Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val
 216 35 40 45
 218 Ser Asp Cys Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu
 219 50 55 60
 221 Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr His Cys His Gln His
 222 65 70 75 80
 224 Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr
 225 85 90 95
 227 Ser Glu Thr Asp Thr Ile Cys Thr Cys Glu Glu Gly Trp His Cys Thr
 228 100 105 110
 230 Ser Glu Ala Cys Glu Ser Cys Val Leu His Arg Ser Cys Ser Pro Gly
 231 115 120 125
 233 Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp Thr Ile Cys Glu
 234 130 135 140
 236 Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser Ala Phe Glu Lys
 237 145 150 155 160
 239 Cys His Pro Trp Thr Ser Cys Glu Thr Lys Asp Leu Val Val Gln Gln
 240 165 170 175
 242 Ala Gly Thr Asn Lys Thr Asp Val Val Cys Gly Pro Gln Asp Arg Leu
 243 180 185 190
 245 Arg Ala Leu Val Val Ile Pro Ile Ile Phe Gly Ile Leu Phe Ala Ile
 246 195 200 205
 248 Leu Leu Val Leu Val Phe Ile Lys Lys Val Ala Lys Lys Pro Thr Asn
 249 210 215 220
 251 Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro Asp
 252 225 230 235 240
 254 Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu His
 255 245 250 255
 257 Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser
 258 260 265 270
 260 Val Gln Glu Arg Gln
 261 275
 264 <210> SEQ ID NO: 6
 265 <211> LENGTH: 735
 266 <212> TYPE: PRT
 267 <213> ORGANISM: Homo sapiens
 269 <400> SEQUENCE: 6
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 271 1 5 10 15
 273 Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu Ser Arg Tyr Leu
 274 20 25 30
 276 Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser Thr Thr Gly Cys
 277 35 40 45
 279 Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp Ser Pro Leu Asn
 280 50 55 60
 282 Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu Thr Met Asn Pro

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283	65	70	75	80													
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288	Ser	Arg	Lys	Leu	Glu	Lys	Gly	Ile	Gln	Val	Glu	Ile	Tyr	Ser	Phe	Pro	
289																	110
291	Lys	Asp	Pro	Glu	Ile	His	Leu	Ser	Gly	Pro	Leu	Glu	Ala	Gly	Lys	Pro	
292																	125
294	Ile	Thr	Val	Lys	Cys	Ser	Val	Ala	Asp	Val	Tyr	Pro	Phe	Asp	Arg	Leu	
295																	140
297	Glu	Ile	Asp	Leu	Leu	Lys	Gly	Asp	His	Leu	Met	Lys	Ser	Gln	Glu	Phe	
298																	160
300	Leu	Glu	Asp	Ala	Asp	Arg	Lys	Ser	Leu	Glu	Thr	Lys	Ser	Leu	Glu	Val	
301																	175
303	Thr	Phe	Thr	Pro	Val	Ile	Glu	Asp	Ile	Gly	Lys	Val	Leu	Val	Cys	Arg	
304																	190
306	Ala	Lys	Leu	His	Ile	Asp	Glu	Met	Asp	Ser	Val	Pro	Thr	Val	Arg	Gln	
307																	205
309	Ala	Val	Lys	Glu	Leu	Gln	Val	Tyr	Ile	Ser	Pro	Lys	Asn	Thr	Val	Ile	
310																	220
312	Ser	Val	Asn	Pro	Ser	Thr	Lys	Leu	Gln	Glu	Gly	Gly	Ser	Val	Thr	Met	
313																	240
315	Thr	Cys	Ser	Ser	Glu	Gly	Leu	Pro	Ala	Pro	Glu	Ile	Phe	Trp	Ser	Lys	
316																	255
318	Lys	Leu	Asp	Asn	Gly	Asn	Leu	Gln	His	Leu	Ser	Gly	Asn	Ala	Thr	Leu	
319																	270
321	Thr	Leu	Ile	Ala	Met	Arg	Met	Glu	Asp	Ser	Gly	Ile	Tyr	Val	Cys	Glu	
322																	285
324	Gly	Val	Asn	Leu	Ile	Gly	Lys	Asn	Arg	Lys	Glu	Val	Glu	Leu	Ile	Val	
325																	300
327	Gln	Glu	Lys	Pro	Phe	Thr	Val	Glu	Ile	Ser	Pro	Gly	Pro	Arg	Ile	Ala	
328																	320
330	Ala	Gln	Ile	Gly	Asp	Ser	Val	Met	Leu	Thr	Cys	Ser	Val	Met	Gly	Cys	
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333	Glu	Ser	Pro	Ser	Phe	Ser	Trp	Arg	Thr	Gln	Ile	Asp	Ser	Pro	Leu	Ser	
334																	350
336	Gly	Lys	Val	Arg	Ser	Glu	Gly	Thr	Asn	Ser	Thr	Leu	Thr	Leu	Ser	Pro	
337																	365
339	Val	Ser	Phe	Glu	Asn	Glu	His	Ser	Tyr	Leu	Cys	Thr	Val	Thr	Cys	Gly	
340																	380
342	His	Lys	Lys	Leu	Glu	Lys	Gly	Ile	Gln	Gly	Glu	Leu	Tyr	Ser	Phe	Pro	
343																	400
345	Arg	Asp	Pro	Glu	Ile	Glu	Met	Ser	Gly	Gly	Leu	Val	Asn	Gly	Ser	Ser	
346																	415
348	Cys	Thr	Val	Ser	Cys	Lys	Val	Pro	Ser	Val	Tyr	Pro	Leu	Asp	Arg	Leu	
349																	430
351	Glu	Ile	Glu	Leu	Leu	Lys	Gly	Glu	Thr	Ile	Leu	Glu	Asn	Ile	Glu	Phe	
352																	445
354	Leu	Glu	Asp	Thr	Asp	Met	Lys	Ser	Leu	Glu	Asn	Lys	Ser	Leu	Glu	Met	
355																	460

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date